

Overview of method for functional site regulatory activity using functional site arrays

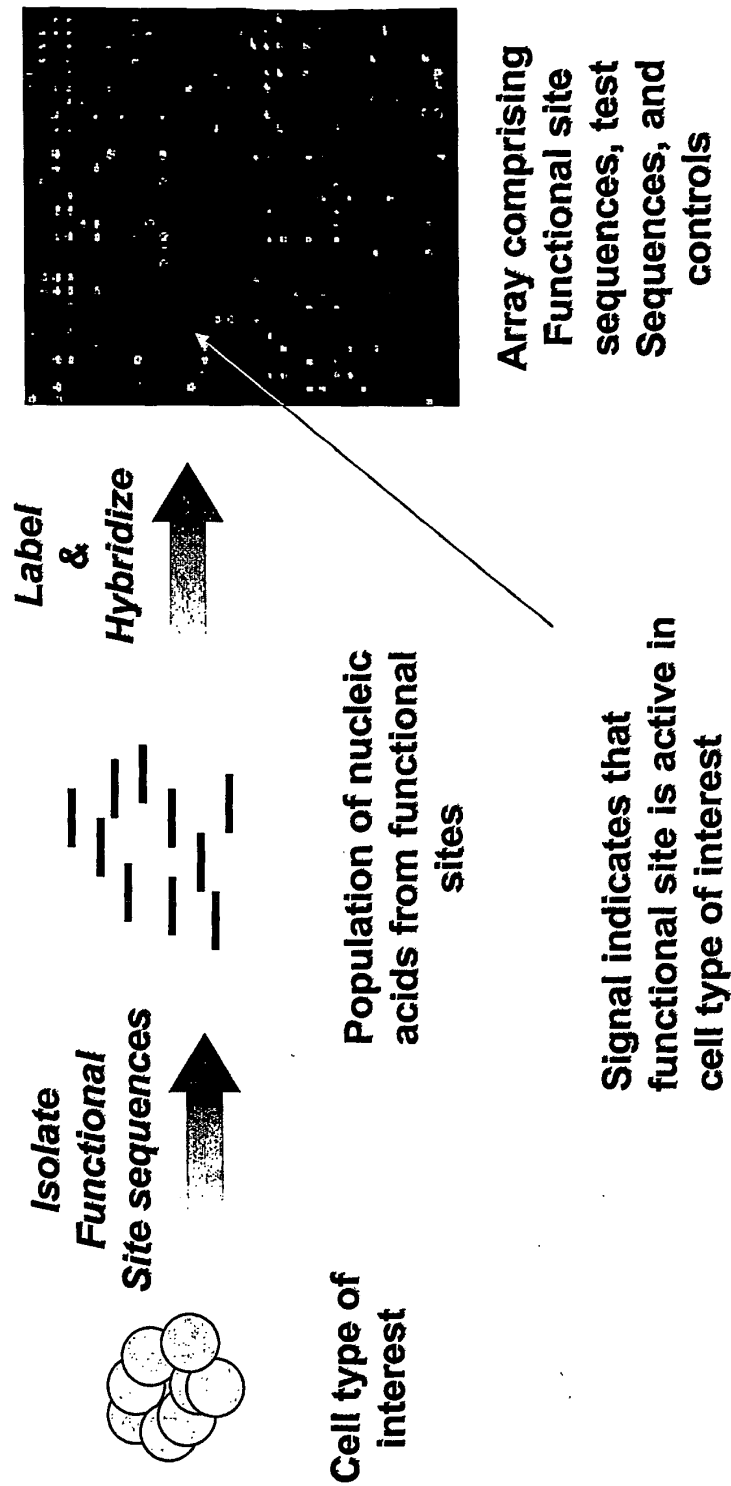


Figure 1

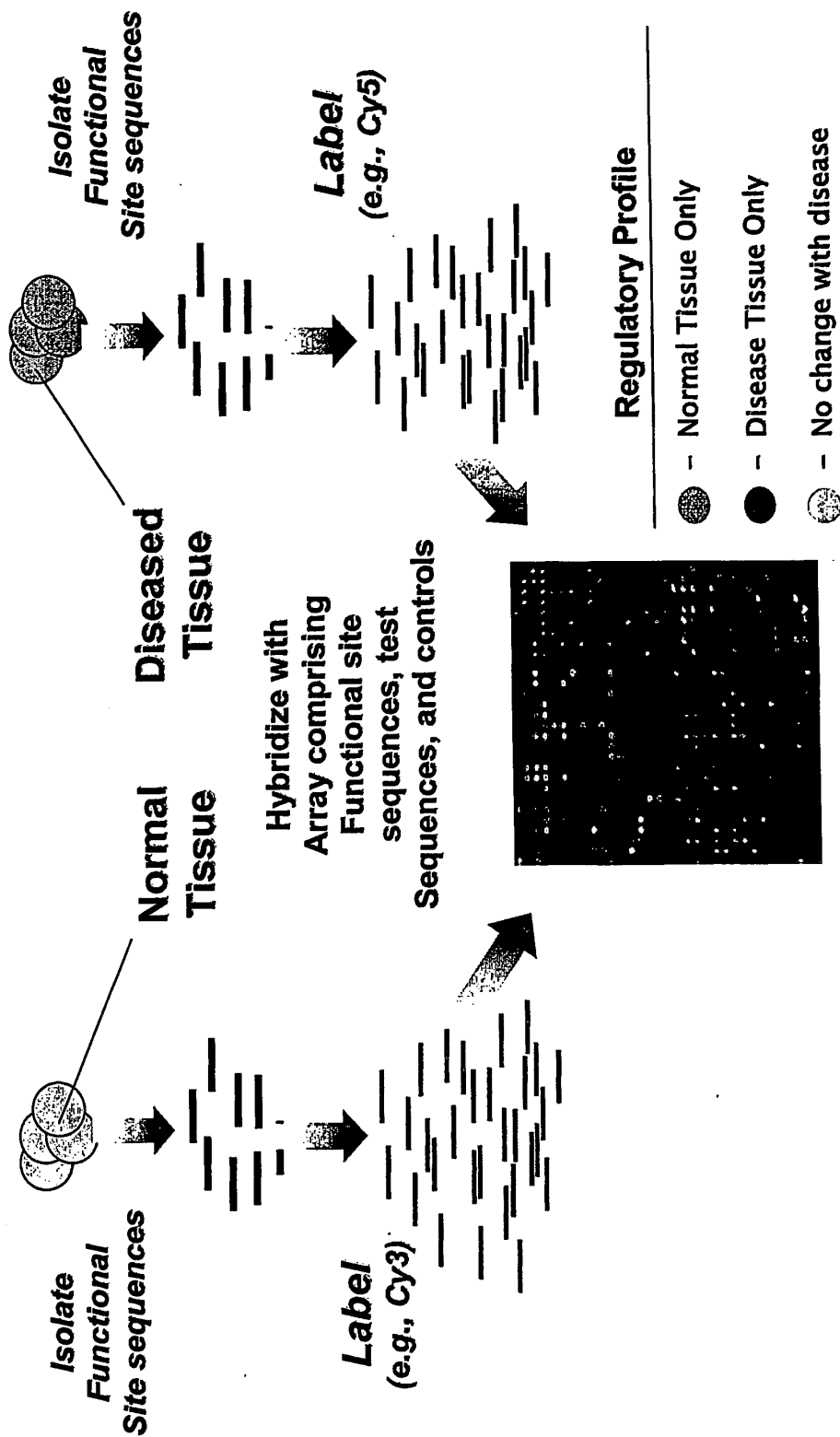


Figure 2

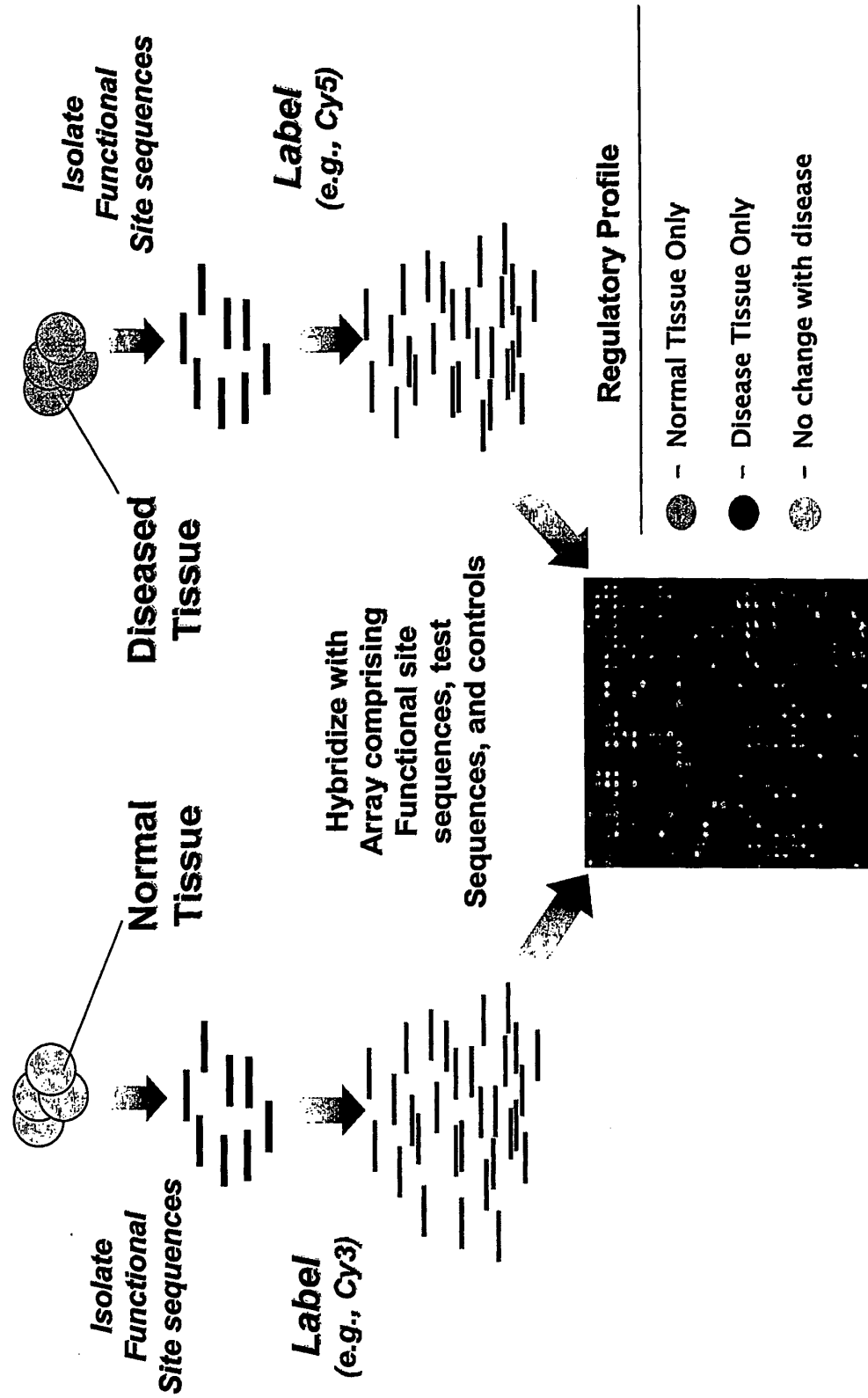


Figure 3

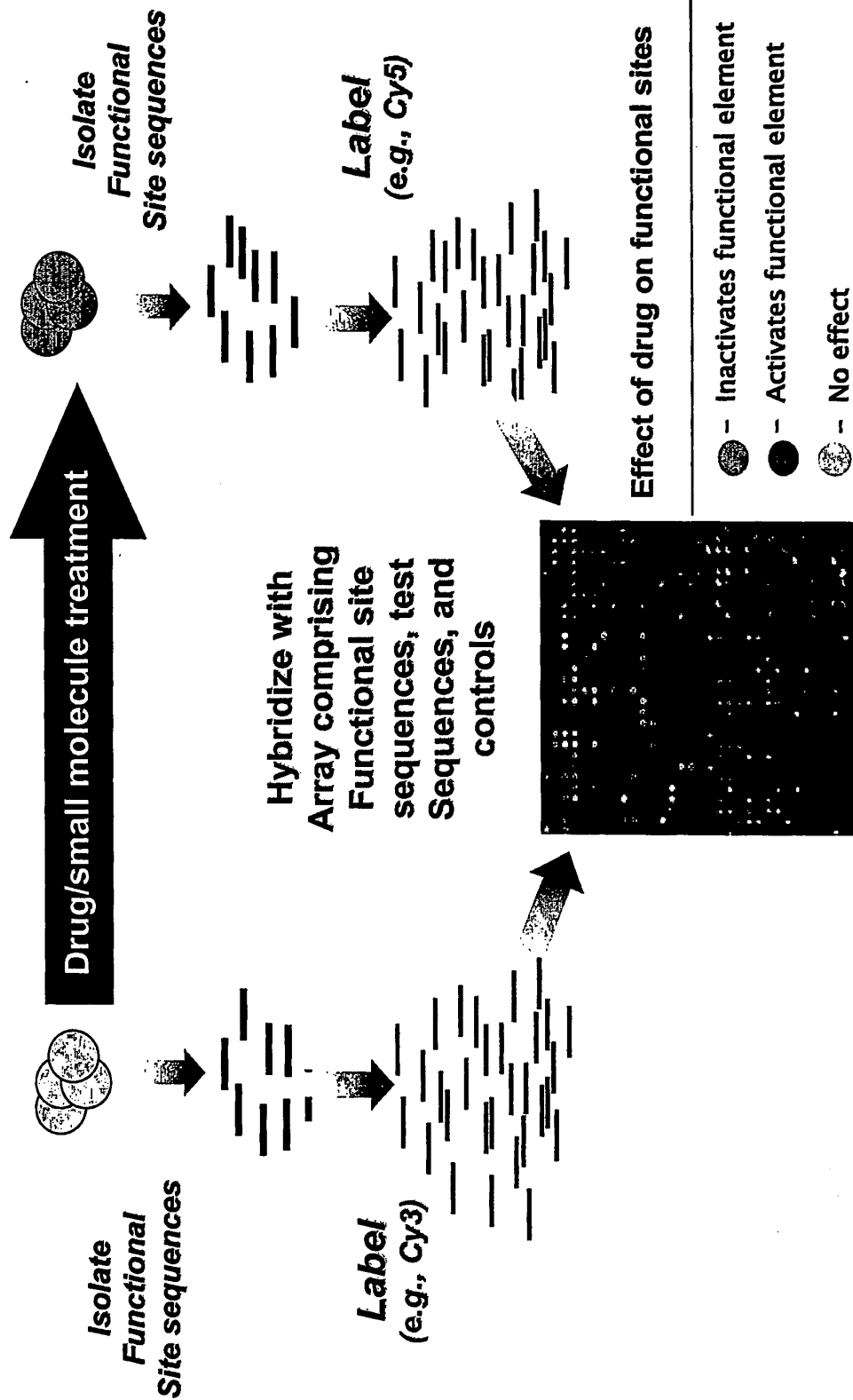
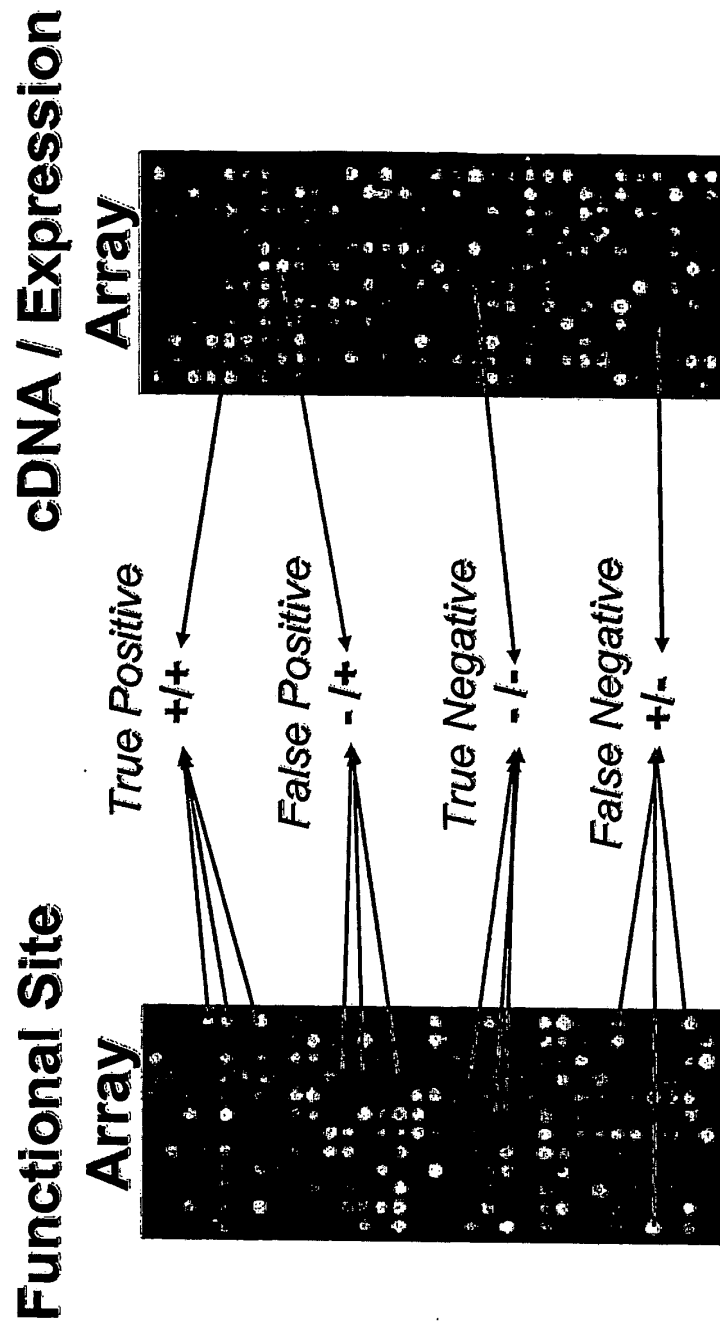


Figure 4

*Figure 5*

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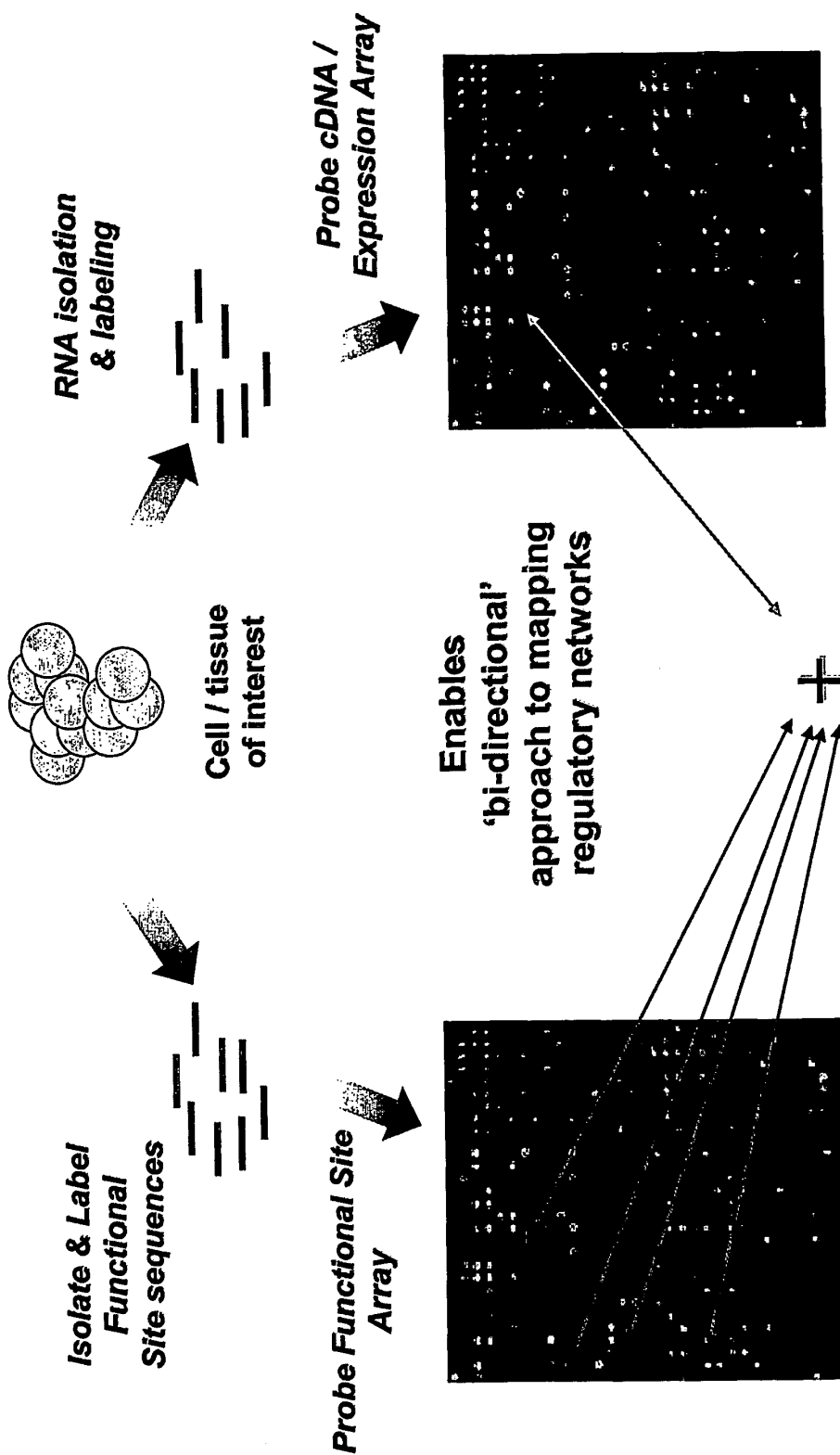


Figure 6

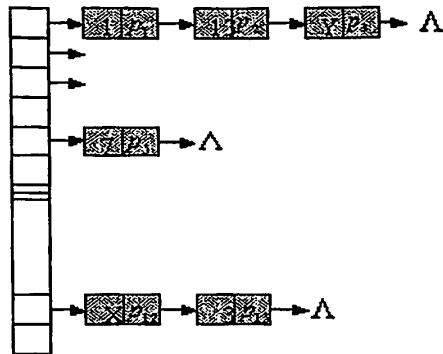


Figure 7

SEQ ID NO:26 GCTGAGAAAACATCAAGCTGTGTTTCTCCTTCCCCAAAGACTTCGC

Minimum or low frequency 16-mer

SEQ ID NO:27 AAGCTGTGTTTCTCCT 5 50883741 0

SEQ ID NO:27 AAGCTGTGTTTCTCCT X 16 0

SEQ ID NO:27 AAGCTGTGTTTCTCCT Y 19550621 0

SEQ ID NO:28 AGGAGAAACACAGCTT 4 88449985 1

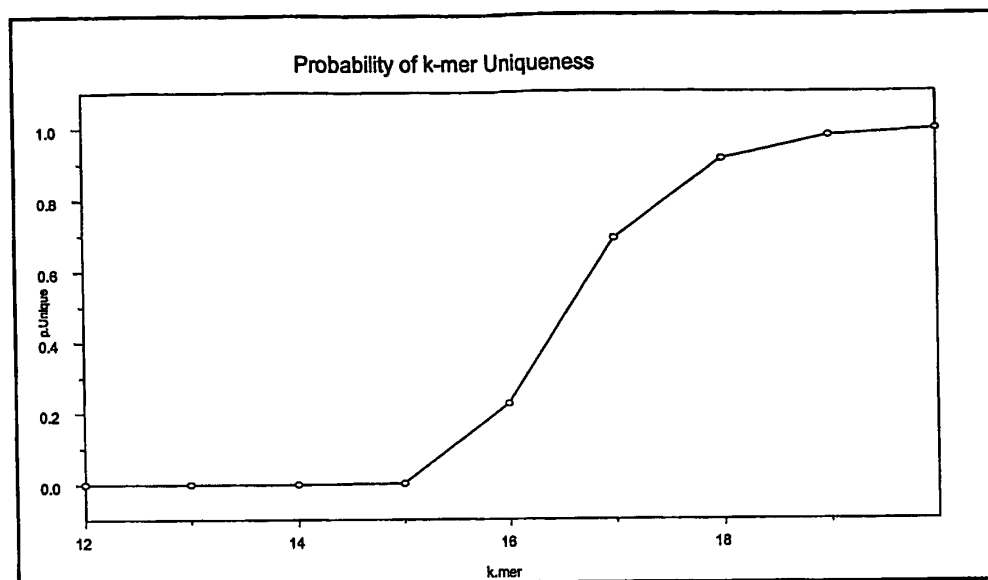
SEQ ID NO:28 AGGAGAAACACAGCTT 18 76567666 1

SEQ ID NO:28 AGGAGAAACACAGCTT 21 33297808 1

SEQ ID NO:28 AGGAGAAACACAGCTT Y 19088526 1

Query genome at appropriate positions for *prefix* and *suffix*

Figure 8

**Figure 9**

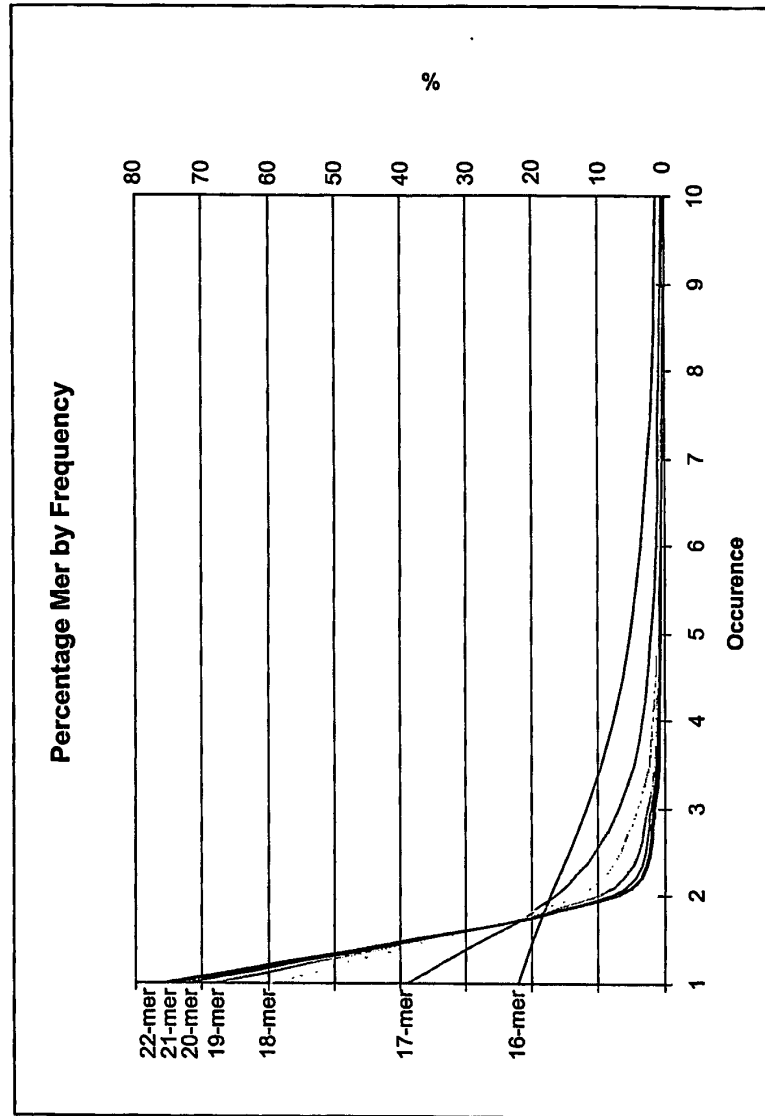
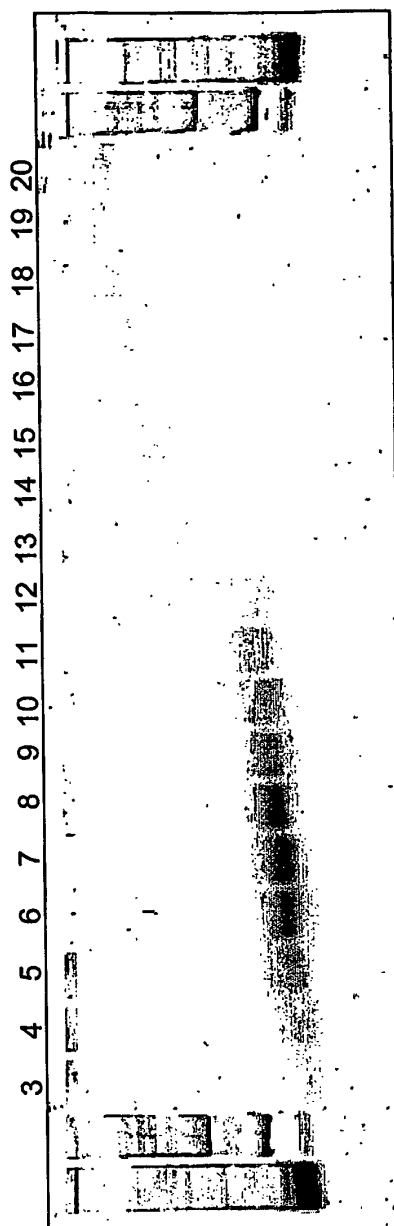


Figure 10

DNA profile in individual fractions (25 ul of 6x540 ul fraction):



Fractions obtained by sucrose-gradient centrifugation 022018 (run #4) of DS-4586 and DS-4587. Run directly from sucrose fractions prior to RNaseA treatment. Total volume of DNA precipitated from fractions and dissolved in LoTE is approx. 80 ul.

Figure 11

Correlation between ScanMer(26) scores with Genomic(K562) Hybridization Avg Nsum Intensity

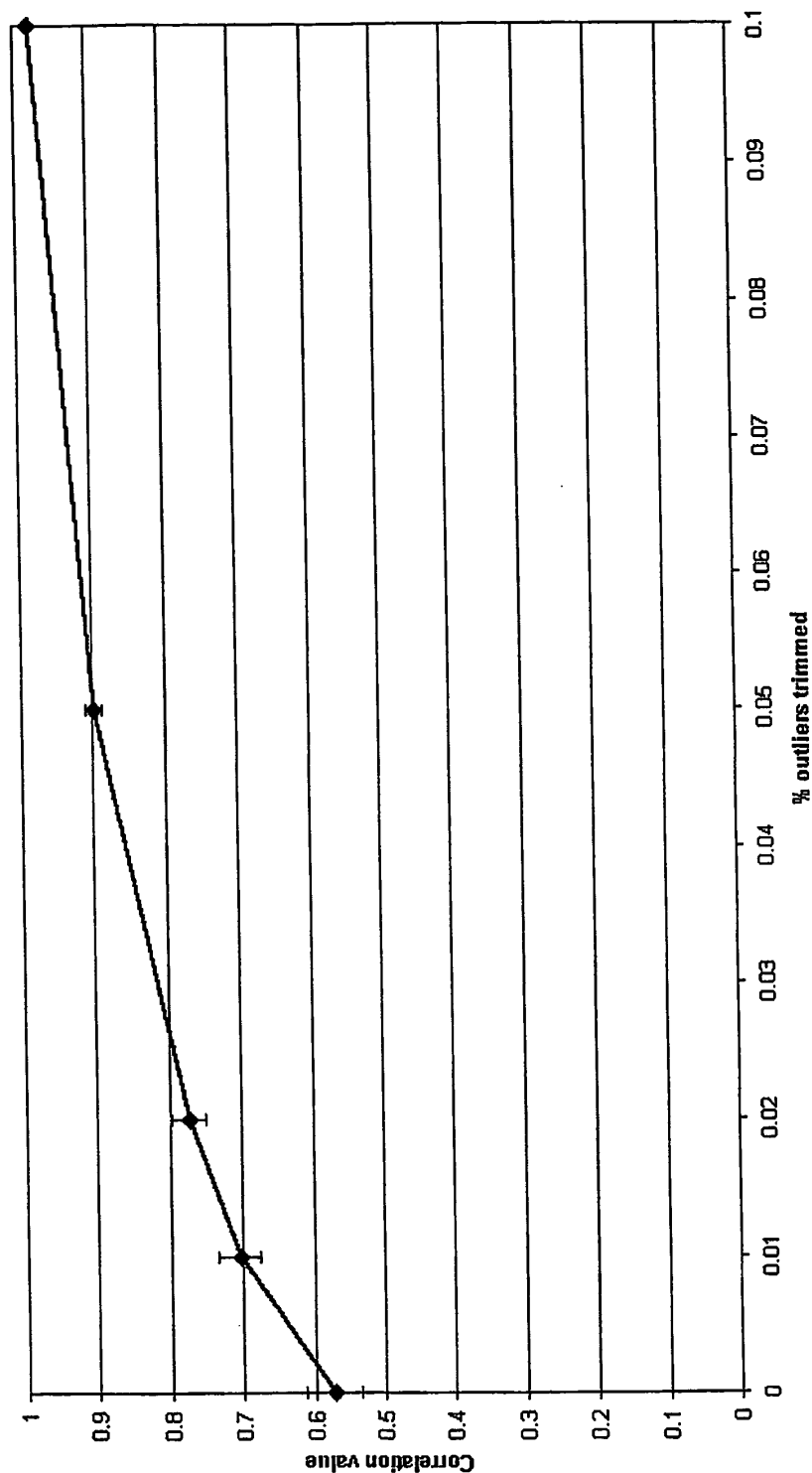


Figure 12

MYC

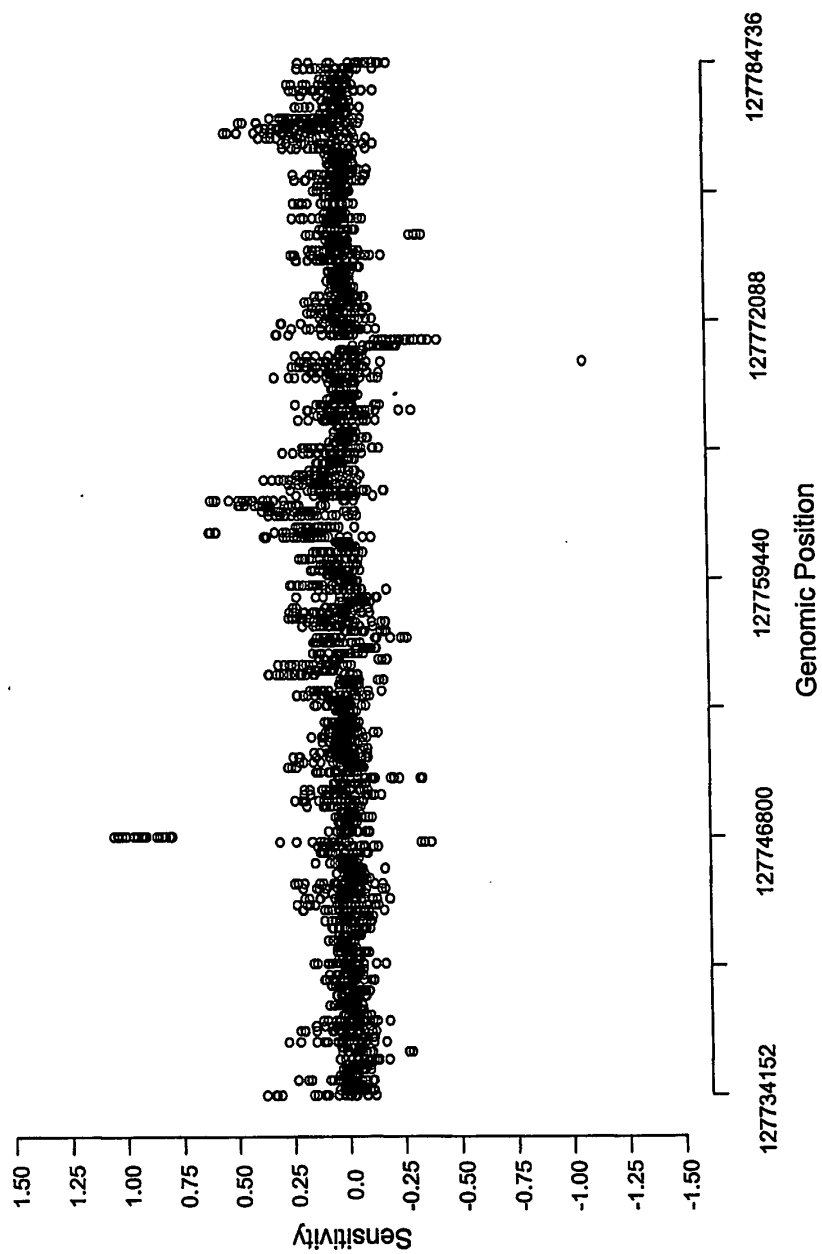


Figure 13.

MYC

WO 2004/052080

10/538733

PCT/US2003/039645

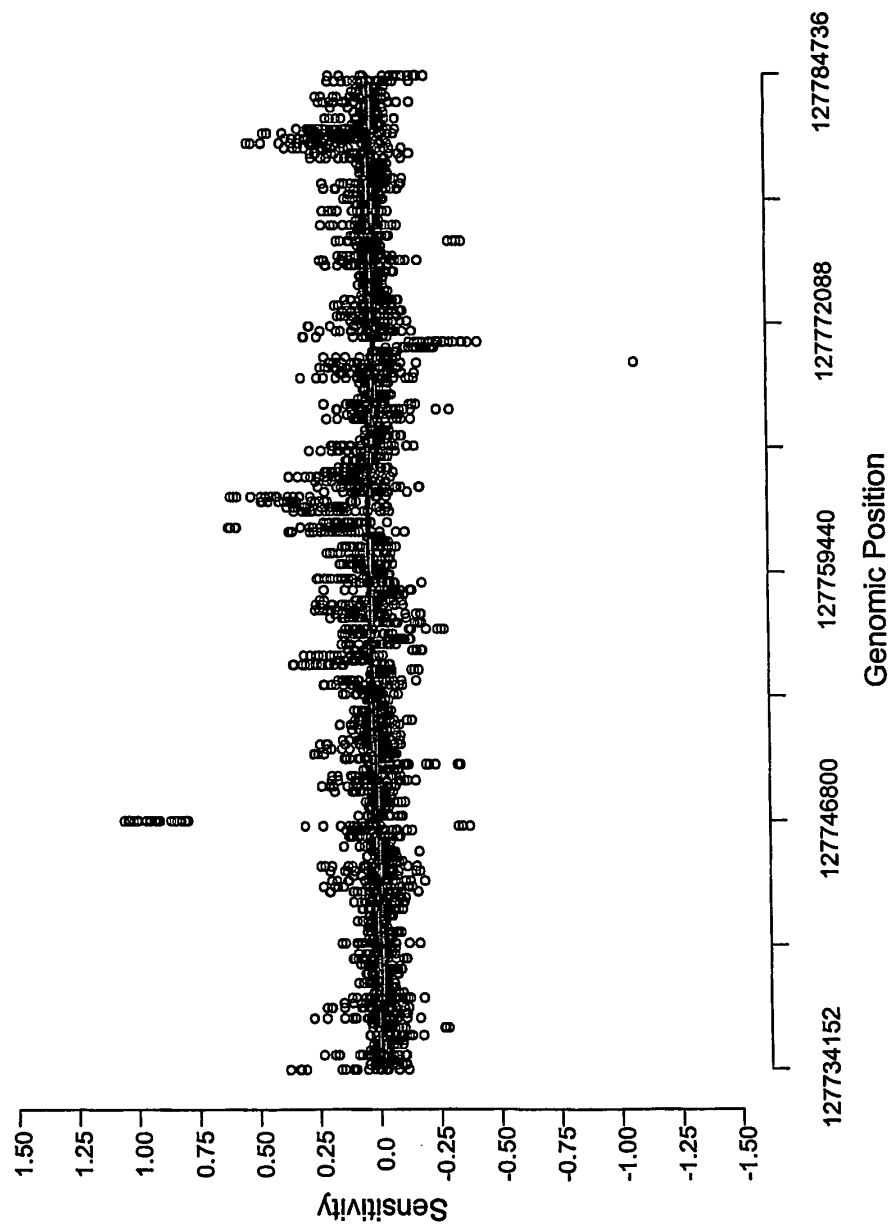


Figure 14.

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MYC

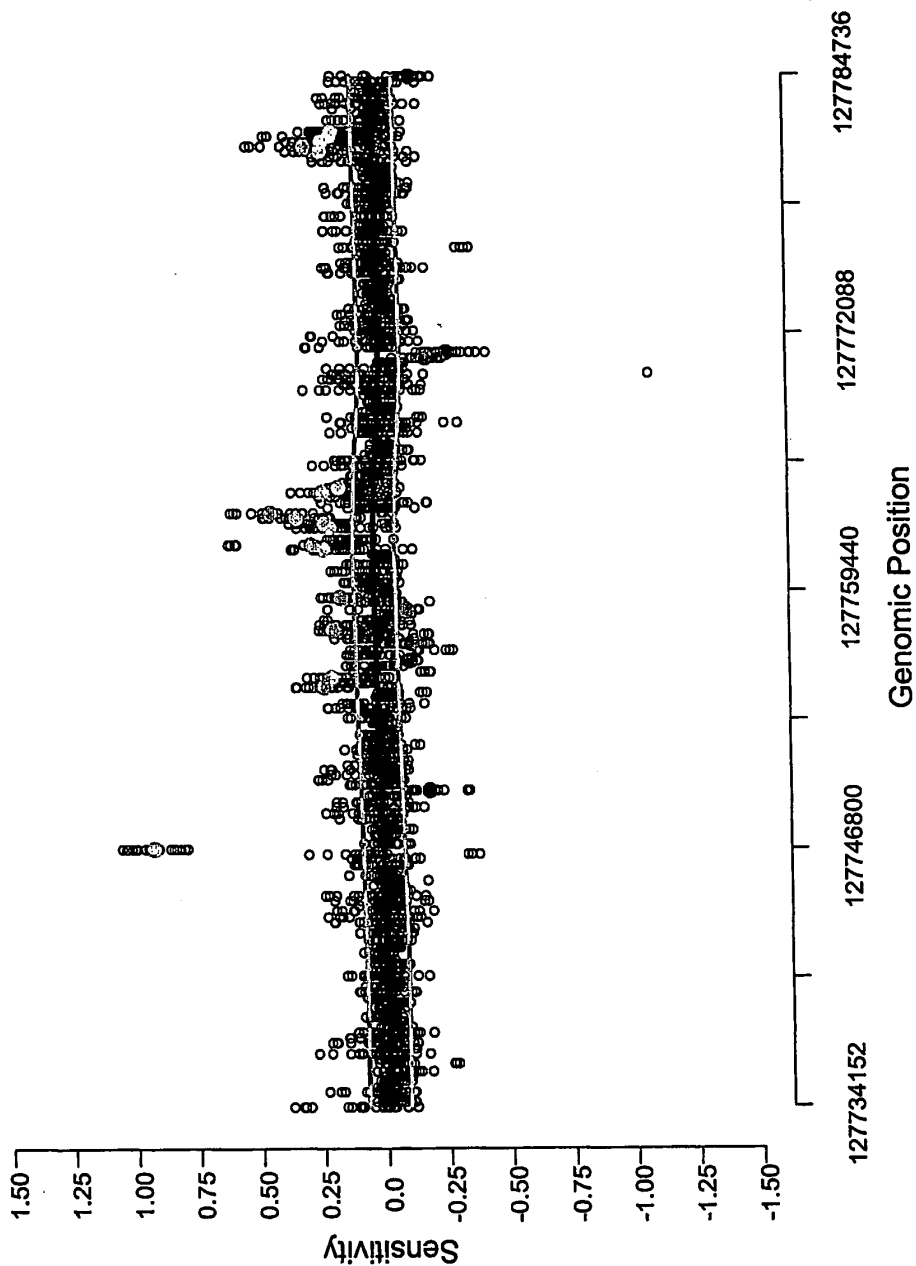


Figure 15.

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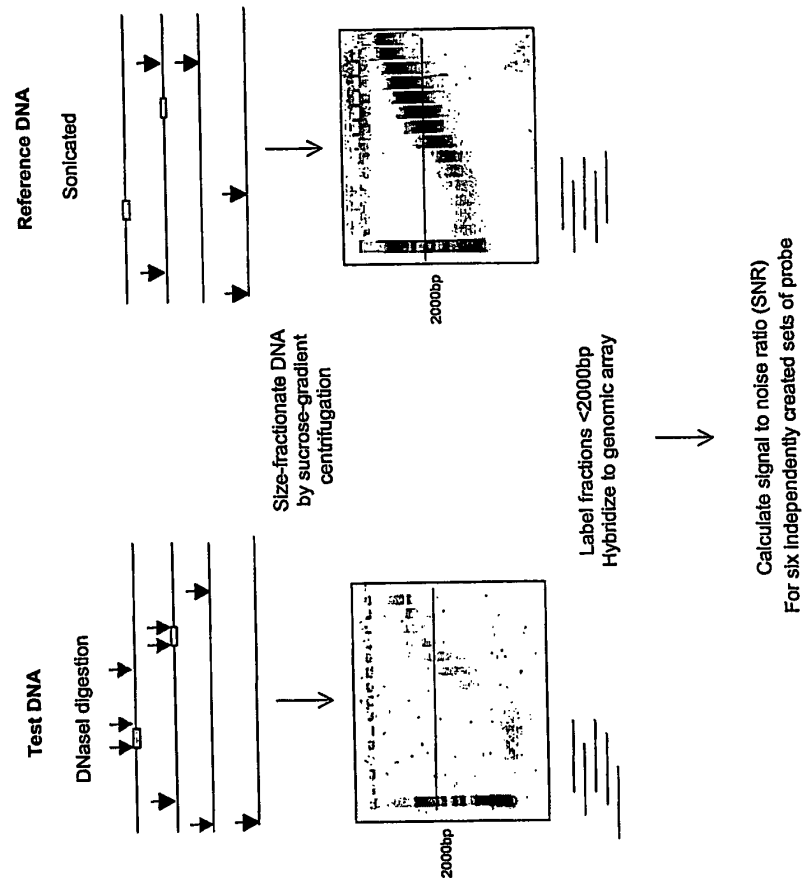


Figure 16.

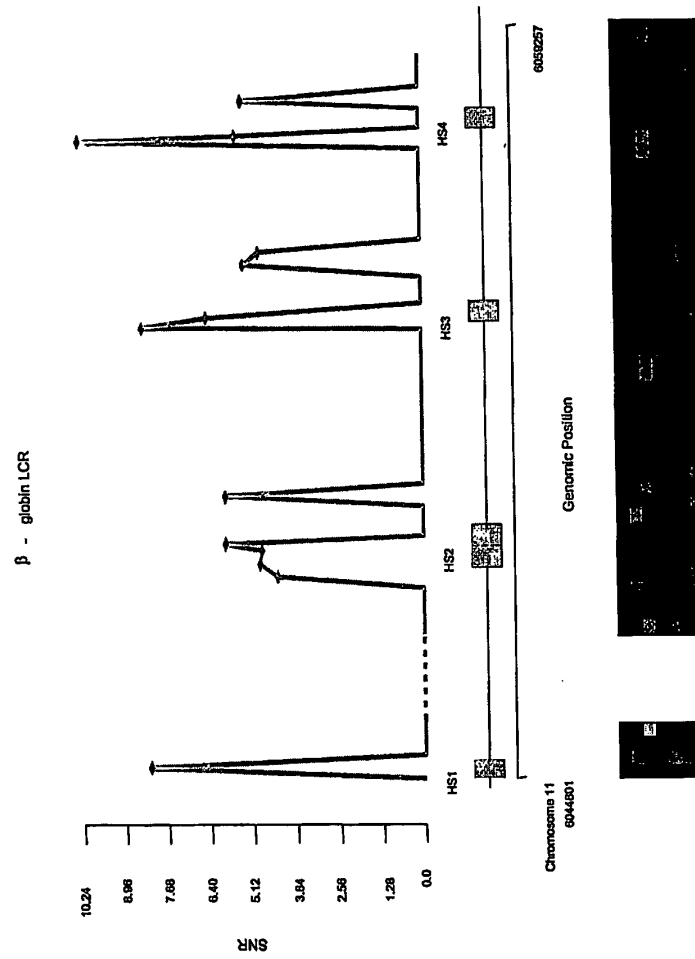


Figure 17

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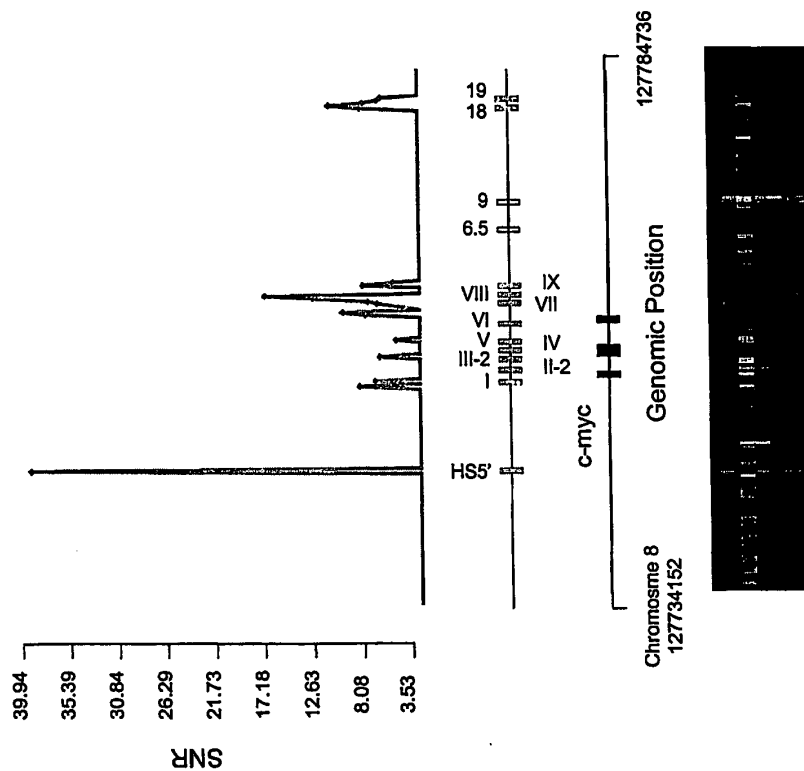


Figure 18.

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